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Essential Role of the Linear Ubiquitin Chain Assembly Complex in Lymphoma Revealed by Rare Germline Polymorphisms

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Abstract

Constitutive activation of NF- κ B is a hallmark of the activated B cell-like (ABC) subtype of diffuse large B cell lymphoma (DLBCL), owing to upstream signals from the B cell receptor (BCR) and MyD88 pathways. The linear polyubiquitin chain assembly complex (LUBAC) attaches linear polyubiquitin chains to I κ B kinase γ , a necessary event in some pathways that engage NF- κ B. Two germ line polymorphisms affecting the LUBAC subunit RNF31 are rare among healthy individuals (~1%) but enriched in ABC DLBCL (7.8%). These polymorphisms alter RNF31 α helices that mediate binding to the LUBAC subunit RBCK1, thereby increasing RNF31-RBCK1 association, LUBAC enzymatic activity, and NF- κ B engagement. In the BCR pathway, LUBAC associates with the CARD11/MALT1/BCL10 adapter complex and is required for ABC DLBCL viability. A stapled RNF31 α -helical peptide based on the ABC DLBCL-associated Q622L polymorphism inhibited RNF31-RBCK1 binding, decreased NF- κ B and killed ABC DLBCL cells, credentialing this protein-protein interface as a therapeutic target.

Introduction

Diffuse large B cell lymphoma (DLBCL) can be divided into two main molecular subtypes, termed activated B cell-like (ABC) and germinal center B cell-like (GCB) DLBCL, which differ in their gene expression profiles, oncogenic abnormalities and clinical behavior(1, 2). In ABC DLBCL, regulatory pathways normally associated with B cell activation are constitutively engaged(1). In particular, the NF- κ B pathway plays an essential role in its pathogenesis by promoting malignant cell survival and inducing expression of the master regulatory transcription factor IRF4(3, 4).

Recent genomic and functional studies have elucidated the molecular mechanisms underlying constitutive NF- κ B activity in ABC DLBCL, highlighting the central role of the B cell receptor (BCR) and MyD88 signaling pathways. The involvement of BCR signaling in ABC DLBCL was first revealed by the dependence of these lymphomas on the adapter protein CARD11(5). In response to BCR signaling, CARD11 forms a multiprotein “CBM” complex with MALT1 and BCL10 and activates I κ B kinase (IKK), thereby triggering the classical NF- κ B pathway. In 10% of ABC DLBCL tumors, CARD11 sustains oncogenic somatic mutations that constitutively activate IKK and NF- κ B(6). In other ABC DLBCLs with wild type CARD11, CARD11 is nonetheless essential for survival, revealing the dependence of these lymphomas on BCR signaling, a phenomenon dubbed “chronic active” BCR signaling(7). In more than 20% of ABC DLBCL cases, mutations in the ITAM motifs of the BCR subunits CD79B and CD79A augment chronic active BCR signaling(7), providing genetic evidence that BCR signaling is central to the pathogenesis of this

lymphoma subtype. A second pathway activating NF- κ B in ABC DLBCL is mediated by MYD88, the central adapter in Toll-like receptor signaling(8). MYD88 silencing is lethal to ABC DLBCL cells due to inhibition of NF- κ B and autocrine IL-6/IL-10 signaling through JAK kinase and STAT3(8, 9). In 39% of ABC DLBCL cases, this pathway is activated by somatic, gain-of-function MYD88 mutations(8). The most common MYD88 mutant, L265P, spontaneously coordinates a signaling complex in which IRAK4 phosphorylates IRAK1, leading to IKK and NF- κ B activation(8).

Protein ubiquitination is involved in various steps of the NF- κ B pathway(10). A recently identified type of polyubiquitin, the linear polyubiquitin chain, plays important roles in NF- κ B activation(11-14). This polyubiquitin chain is generated by linkages between the C- and N-terminal amino acids of ubiquitin modules, resulting in a head-to-tail linear polyubiquitin polymer. The E3 ligase complex responsible for linear polyubiquitin chain formation is the linear ubiquitin chain assembly complex (LUBAC), composed of RNF31 (HOIP), RBCK1 (HOIL-1L), and SHARPIN. In the canonical NF- κ B pathway, LUBAC specifically recognizes and conjugates linear polyubiquitin chains onto the IKK γ /NEMO subunit, which is considered to be an essential event that activates of IKK and NF- κ B(11, 15). Cells derived from both *cpdm* (SHARPIN mutant) and *HOIL-1L*^{-/-} mice have reduced activation of the canonical NF- κ B pathway in response to multiple stimuli and as well as increased TNF α -induced apoptosis, highlighting the critical role of LUBAC in NF- κ B activation(11-14). Although the full physiological function of LUBAC is still largely unknown, it appears to regulate B cell function and innate immune responses(12, 13, 16-19). The fact that the BCR and MYD88 signaling pathways are recurrently targeted by genetic changes in ABC DLBCL suggest that the constitutive activation of NF- κ B in this malignancy could depend on LUBAC function.

Although NF- κ B is an attractive therapeutic target in ABC DLBCL, no IKK inhibitors have been developed for clinical use due to concerns regarding the pleiotropic effects of IKK and potential on-target toxicities. Unlike mice with disruption of the genes encoding IKK β or NEMO, which succumb to massive liver cell death, knockout animals for the LUBAC component RBCK1 are born healthy, suggesting that therapies targeting this pathway might have tolerable side effects. Since ABC DLBCL is the subtype of DLBCL that is most refractory to current therapy(20), new therapeutic strategies are needed. In the present report, we investigate the role of LUBAC in ABC DLBCL and its potential as a therapeutic target.

Results

Enrichment of two rare SNPs among ABC DLBCL tumors

Given the importance of LUBAC activity in NF- κ B signaling, we searched for mutations affecting LUBAC components using RNA-seq data from ABC DLBCL biopsies and identified two recurrent missense mutations that change glutamine 584 to histidine (Q584H; n=2) and glutamine 622 to leucine (Q622L; n=3). Both of these mutations have been identified previously as rare SNPs: among the healthy individuals studied in the 1000 Genomes Project (n=1094)(21) and GO Exome Sequencing Project (n=8413)(22), Q584H (SNP accession rs184184005) had a minor allele frequency (MAF) of 0.19% and 0.13%,

respectively, whereas Q622L (SNP accession rs149481717) had a MAF of 0.24% and 0.49%, respectively. Both SNPs are located in a highly conserved region of *RNF31* that encodes the ubiquitin-associated (UBA) domain, which interacts with the ubiquitin-like (UBL) domain of RBCK1, leading to LUBAC enzyme formation(11, 23) (Fig. 1a and Fig. 1b).

We resequenced *RNF31* exon 10, which includes these SNPs, in 561 biopsy samples of various lymphoma subtypes. In 103 ABC DLBCL biopsies, we detected Q584H in 2 cases (1.94%) and Q622L in 6 cases (5.83%), with an overall frequency of 7.77% (3.41%-14.73%, 95% C.I.), which is 8.22-fold (4.05-16.65, 95% C.I.) higher than in healthy individuals studied in the GO Exome Sequencing Project(22) and the 1000 Genomes Project(21) ($p=1.02 \times 10^{-5}$) (Fig. 1c, Supplementary Table 1). Among 458 samples of other lymphoid malignancies, 3 Q622L cases were identified, one each in the GCB subtype of DLBCL, follicular lymphoma, Hodgkin lymphoma, and no cases had Q584H, yielding a frequency of both SNPs in non-ABC DLBCL cases of 0.66%, which is similar to the frequency in the healthy cohorts (0.95%), but 11.9-fold lower than the frequency in ABC DLBCL ($p=1.03 \times 10^{-4}$). Of note, all of the ABC DLBCL cases carrying these SNPs had either a MYD88 mutation or genetic aberrations affecting A20, while only one had a mutation in the CD79B subunit of the BCR (Supplementary Table 2). In five ABC DLBCL cases with available germ line DNA, both Q584H and Q622L were confirmed to be germline variants (Supplementary Fig. 1).

LUBAC is essential for NF- κ B activity in ABC DLBCL

RNA interference-mediated depletion of RNF31 and SHARPIN was toxic for most of ABC DLBCL lines but had little effect on the GCB DLBCL lines tested (Fig. 2a). The attachment of linear ubiquitin chains to the IKK γ /NEMO subunit is required for NF- κ B activity in response to various stimuli(11, 15). In ABC DLBCL cells, NEMO was constitutively modified by polyubiquitin, and depletion of RNF31 or SHARPIN decreased this modification (Fig. 2b). Accordingly, depletion of these LUBAC components decreased two indicators of IKK activity, phosphorylation of IKK β and its substrate I κ B α (Fig. 2b). The activity of IKK β can be measured using a reporter construct in which I κ B α is fused to luciferase(24). Knockdown of RNF31 in an ABC DLBCL line caused a rise in the I κ B α -luciferase reporter, indicating IKK β inhibition (Fig. 2c). Likewise, RNF31 and SHARPIN depletion decreased nuclear NF- κ B p65 DNA binding (Fig. 2d) and RNF31 depletion reduced NF- κ B transcriptional activity in ABC DLBCL, as indicated by a luciferase reporter driven by an NF- κ B response element (Fig. 2e). Hence, LUBAC is essential for maintaining NF- κ B activity and viability of ABC DLBCL cells.

Role of LUBAC in CBM complex-mediated NF- κ B activation

We next investigated the role of LUBAC in the BCR and MyD88 pathways, which govern NF- κ B activity in ABC DLBCL. By co-immunoprecipitation, RNF31 associated with MALT1 and, to a lesser extent, IRAK1 in ABC DLBCL lines, suggesting that the LUBAC complex could play a role in both pathways (Fig. 3a). Using an antibody specific for linear ubiquitin(11, 13), this modification was detectable on IKK γ /NEMO immunoprecipitated from ABC DLBCL cells, as expected, but also on IRAK1 (Supplementary Fig. 2). Neither

protein was modified by linear ubiquitin in the control GCB DLBCL line. By contrast, linear ubiquitin was not detectable in immunoprecipitates of MALT1 or CARD11.

Chronic active BCR signaling in ABC DLBCL causes MALT1 to proteolytically cleave A20, a negative regulator of NF- κ B signaling(25, 26). Knockdown of RNF31 decreased A20 proteolysis in ABC DLBCL lines, implicating LUBAC in this regulatory process (Fig. 3b). Acute BCR cross-linking by anti-IgM antibodies in a GCB DLBCL line (BJAB) or in an ABC DLBCL line (HBL1) rapidly increased IKK β phosphorylation, but knockdown of RNF31 compromised this induction, reinforcing the view that LUBAC plays a key role in NF- κ B activation during BCR signaling (Fig. 3c and Supplementary Fig. 3a). In keeping with these results, ABC DLBCL lines depleted of RNF31 were sensitized to the BTK kinase inhibitor ibrutinib, which blocks chronic active BCR signaling in ABC DLBCL(7), and to lenalidomide, which reduces CARD11 levels by inhibiting IRF4(4) (Fig. 3d and Supplementary Fig. 3b). Together, these results show that LUBAC is associated with the CBM complex and contributes to BCR signaling in ABC DLBCL cells.

RNF31 SNPs promote NF- κ B activity in ABC DLBCL

A small region of the RNF31 UBA domain, from amino acids 579 to 623, binds to the UBL domain of RBCK1(23). The RNF31 Q584H and Q622L mutants reside in this region, suggesting that they might promote LUBAC complex formation and subsequent NF- κ B activation. When these RNF31 mutants or wild type RNF31 were expressed in ABC DLBCL cells at equivalent levels, Q622L and Q584H increased the activity of an NF- κ B-driven luciferase reporter more effectively than wild-type RNF31 (Fig. 4a). Expression levels of two well-known NF- κ B target genes, *NFKBIA* and *IRF4*, were elevated by the RNF31 mutants more than by wild type RNF31 (Fig. 4b). The RNF31 mutants were also more active in stimulating IKK activity than wild type RNF31, as judged by the I κ B α -luciferase reporter (Fig. 4c) and accordingly were also superior in stimulating phosphorylation of IKK β and its substrate I κ B α (Fig. 4d), and in inducing nuclear NF- κ B p65 DNA binding activity (Fig. 4e). When expressed in the GCB DLBCL BJAB, the RNF31 mutants induced expression of the NF- κ B target gene CD83, especially in response to anti-IgM-induced BCR activation (Fig. 4f), supporting the notion that LUBAC contributes to BCR-induced engagement of NF- κ B (Fig. 3c and Supplementary Fig. 3a).

In keeping with this hypothesis, RNF31 mutants were more effective than wild type RNF31 in stimulating MALT1-dependent cleavage of A20 in ABC DLBCL cells (Fig. 4g). While both mutant and wild type RNF31 isoforms interacted with MALT1 equivalently, A20 was more effectively recruited to the CBM complex in ABC DLBCL cells expressing mutant RNF31 than in cells expressing wild type RNF31 (Fig. 4h). Recent reports demonstrated that zinc finger 7 of A20 binds linear polyubiquitin chains preferentially, thereby facilitating its recruitment to receptor signaling complexes containing LUBAC and IKK(27, 28). In light of this, our results suggested that the RNF31 mutants may promote A20 cleavage by stimulating LUBAC ubiquitination activity and increasing A20 recruitment to the CBM complex.

RNF31 SNPs enhance LUBAC formation and E3 ligase activity

To investigate the possibility that the RNF31 mutants have elevated E3 ligase activity, we studied LUBAC-mediated ubiquitination of IKK γ /NEMO, a modification that is necessary for IKK activation(11). RNF31 depletion decreased the constitutive NEMO linear ubiquitination in the HBL1 ABC DLBCL line, and the RNF31 mutants were more effective in restoring NEMO linear ubiquitination than wild type RNF31 (Fig. 5a). We next transduced HBL1 ABC DLBCL cells with Myc epitope-tagged wild type or mutant RNF31 isoforms and evaluated E3 ligase activity in anti-Myc immunoprecipitates using an ELISA-based assay as well as in an *in vitro* polyubiquitin chain formation assay. While Myc-tagged wild type RNF31 immunoprecipitates had ubiquitin ligase activity, LUBAC complexes formed with Myc-tagged RNF31 mutants were more active (Fig. 5b, 5c). The enzyme activity of LUBAC largely relies on the interaction between RNF31 and RBCK1(29, 30), suggesting that the RNF31 mutants might increase LUBAC formation. By co-immunoprecipitation, the RNF31 Q662L and Q584H interacted 2.07-fold and 1.4-fold more effectively with RBCK1, respectively, than did wild type RNF31 ($p<0.0001$; Fig. 5d, 5e).

Targeting the RBCK1-RNF31 interface with stapled α -helical RNF31 peptides

We next considered the possibility that the RBCK1-RNF31 interaction surface that is altered by the RNF31 polymorphisms could be a therapeutic target. To address this, we synthesized a series of peptides modeled on RNF31 α -helices 8 and 9 (Fig. 1a, b) that reside at the RBCK1-RNF31 interface, using “hydrocarbon stapling”(31) to stabilize their α -helical structure (Fig. 6a). Stapling of the amino-terminal α -helix 8 in the RNF31 wild type and Q622L peptides increased their α -helical character, as expected (Fig. 6b). In cultures of HBL1 cells exposed to fluorescein isothiocyanate (FITC)-conjugated derivatives of these peptides, all cells internalized these peptides to roughly equivalent levels, as judged by flow cytometry and confocal microscopy (Supplementary Fig. 4a; 4b). The ability of these FITC-conjugated peptides to bind to recombinant RBCK1 *in vitro* was examined quantitatively using fluorescence polarization spectroscopy. While both stapled peptides interacted more strongly with RBCK1 than did the unstapled peptide, the stapled FITC-RNF31 N-Q622L peptide was clearly superior to the stapled wild type RNF31 peptide (Fig. 6c). We next set up a competition assay in which binding of FITC-RNF31 N-Q622L to RBCK1 was inhibited by increasing concentrations of unlabelled peptides. Based on the difference in IC₅₀ values, the NQ622L RNF31 peptide had an ~6-fold higher relative affinity for RBCK1 than the wild type RNF31 peptide (Fig. 6d), in keeping with the previous co-immunoprecipitation results (Fig. 5d).

Biological effects of RNF31 stapled peptides in ABC DLBCL

The N-Q622L peptide prevented endogenous LUBAC formation in ABC DLBCL cells to a greater degree than wild type RNF31, as judged by RNF31 co-immunoprecipitation with RBCK1, and the unstapled peptide had little if any effect (Supplementary Fig. 5a). NF- κ B pathway activity in ABC DLBCL cells, as measured by the I κ B α -luciferase assay for IKK β activity and the NF- κ B-driven luciferase reporter, was inhibited by the stapled peptides, with the N-Q622L being more active than N-WT, whereas the unstapled peptide and an unrelated stapled peptide were inactive (Figs. 7a, 7b). RNF31 N-Q622L killed two ABC

DLBCL lines in a dose-dependent fashion but had no toxicity for two GCB DLBCL lines (Fig. 7c). Ectopic expression of a constitutively active IKK β mutant mitigated the effects of RNF31 N-Q622L on ABC DLBCL viability, consistent with IKK being a major target of LUBAC activity in this lymphoma subtype (Supplementary Fig. 5b). Moreover, this stapled peptide sensitized ABC DLBCL lines to the lethal effects of the BTK inhibitor ibrutinib (Fig. 7c). Besides promoting the survival of ABC DLBCL cells, the NF- κ B pathway is well known to inhibit the cytotoxic action of chemotherapy(32). Furthermore, NF- κ B is activated by chemotherapy-induced DNA damage(33), and LUBAC activity is essential for this stress response(34). In keeping with these reports, depletion of RNF31 in ABC DLBCL cells impaired NF- κ B activation in response to the topoisomerase inhibitor etoposide, as measured by phosphorylation of IKK β and I κ B α , while ectopic provision of either of the RNF31 mutants restored the NF- κ B response to a greater extent than wild type RNF31 (Fig. 7d). The RNF31 stapled peptides cooperated with etoposide in killing ABC DLBCL cells, with the N-Q622L stapled peptide having more activity than the wild type version (Fig. 7e).

Discussion

We report two rare germ line polymorphisms affecting the LUBAC subunit RNF31 that were enriched among patients with ABC DLBCL relative to patients with other lymphoma subtypes and to healthy individuals. This genetic observation uncovered an essential role for LUBAC enzyme function in maintaining constitutive NF- κ B activity in ABC DLBCL cells, which is the central feature of its pathogenesis. The ABC DLBCL-associated SNPs, which alter the domain of RNF31 that interacts with RBCK1, enhance LUBAC complex formation, ubiquitin ligase activity, and stimulation of the NF- κ B pathway. We credentialed the RNF31-RBCK1 interface as a therapeutic target using stapled α -helical peptides based on the RNF31 SNPs. This work highlights the potential for rare SNPs in the human population to play a pathogenic role in human disease.

The ABC DLBCL-associated SNPs promote LUBAC formation and the ubiquitin E3 ligase activity. Although the exact mechanism by which these SNPs affect LUBAC activity will require structural studies, their position in the available RNF31-RBCK1 crystal structure offers some insight. The RNF31 Q622L mutant is located in an unusual, bent α -helical region that makes direct contacts with RBCK1(23). Based on analysis of other proteins(35), the proline residue at position 619 would be predicted to create a 26° bend between the two adjacent α -helices, but the observed angle in RNF31 is ~53°. This acute bend appears to be reinforced by electrostatic interactions between glutamic acid 618 (E618) and both Q622 and arginine 621. The non-polar leucine residue introduced by the Q622L polymorphism should not interact with E618 in this way, allowing the carboxy-terminal α -helix to adopt an alternative orientation with respect to RBCK1 and potentially promoting the observed stronger interaction between RNF31 and RBCK1. The Q584H polymorphism, which was functional weaker than Q622L, is nonetheless located in the α 6 helix that makes contact with the bent α 8/ α 9 helix containing Q622. Q584 sits at a sharp kink between the α 6 and α 7 helices, making contact with E591. Conceivably, the introduction of a histidine at position 584 could alter this arrangement and indirectly affect the interaction of the α 8/ α 9 helix with RBCK1.

The present study describes a new role for LUBAC in the CBM complex, whereby LUBAC promotes MALT1 cleavage of A20 during BCR signaling, presumably contributing to greater IKK activity. LUBAC co-immunoprecipitated with MALT1 in ABC DLBCL cells and was required for full IKK activity following BCR cross-linking in a GCB DLBCL line. The association of MALT1 with its substrate A20 was enhanced by expression of RNF31, and mutant RNF31 isoforms that promote greater LUBAC activity increased MALT1/A20 association. One model to explain these observations would be that LUBAC-mediated ubiquitin of protein(s) in the CBM complex attracts A20, owing to the ability of A20 to bind linear ubiquitin(28), thereby increasing the access of MALT1 to its substrate. Although neither MALT1 nor CARD11 was detectably modified by linear ubiquitin, IKK itself could attract A20 to the CBM complex since it was heavily modified by linear ubiquitin and is an integral component of this complex in ABC DLBCL cells(6). Alternatively, LUBAC-mediated ubiquitination in the CBM complex could increase the intrinsic proteolytic activity of MALT1, by an unknown mechanism.

Previous studies have implicated LUBAC in various signaling pathways that engage NF- κ B, including those triggered by TNF, IL-1 β , CD40 ligand (CD40L)(11, 12, 14, 15). In the TNFR1-mediated pathway, LUBAC is recruited to the receptor complex in a TRAF2/c-IAP1/2-dependent fashion by binding to c-IAP1/2-generated ubiquitin linkages(15). Thus, it is likely that LUBAC is recruited to the CBM complex via polyubiquitin chains attached to one or more subunits in this complex. Indeed, the CBM subunits MALT1 and BCL10 are modified by ubiquitin following T cell receptor stimulation(36-38). Moreover, MALT1 is monoubiquitinated in ABC DLBCL cells, and this modification promotes their survival(38). Chronic active BCR signaling in ABC DLBCL presumably stimulates MALT ubiquitination in ABC DLBCL, but the mechanism by which this occurs remains to be elucidated.

Targeting the RNF31-RBCK1 interface using stapled α -helical RNF31 peptides specifically kills ABC DLBCL cells, supporting the development of LUBAC inhibitors for the therapy of ABC DLBCL. Despite the oncogenic role of many E3 ligases in cancer, small molecule inhibitors of the active site of these enzymes have not yet emerged as therapies. Our work suggests that focusing small molecule screens on the RNF31-RBCK1 interface might be a useful strategy. LUBAC inhibitors would be expected to have direct cytotoxic effects on the malignant ABC DLBCL cells but also, by inhibiting NF- κ B, sensitize these cells to the apoptotic effects of conventional chemotherapeutic agents(32). Indeed, the RNF31 stapled peptides sensitized ABC DLBCL cells to etoposide. Our studies also suggest that LUBAC inhibitors should sensitize ABC DLBCLs to targeted agents that affect the NF- κ B pathway, including ibrutinib and lenalidomide. When contemplating LUBAC as a therapeutic target, it is important to emphasize that LUBAC appears to participate in some, but not all, signaling events that activate IKK and NF- κ B. In particular, mice with mutations that disrupt LUBAC components do not phenocopy mice with loss of IKK β or IKK γ , which are characterized by massive liver apoptosis during development(11-14). Likewise, a rare inherited human immunodeficiency disease caused by loss-of-function *RBCK1* mutations was characterized by loss of NF- κ B activation in some cell types but gain of NF- κ B activity in others(39). Thus, drugs targeting LUBAC would have a different spectrum of activities than IKK β

inhibitors. Given the presumed importance of BCR and TLR signaling in autoimmune/inflammatory diseases(40), LUBAC inhibitors might prove useful beyond ABC DLBCL.

Finally, our study demonstrates the value of interrogating rare germ line polymorphisms for their role in cancer. Recent examples of rare germ line polymorphisms contributing to tumorigenesis have been described in neuroblastoma and melanoma(41-44). These alleles are difficult to discover by standard genome-wide association methods, but can confer a high relative risk, as is the case for the RNF31 polymorphisms in ABC DLBCL. Our study highlights the importance of functional analysis in evaluating the contribution of rare SNPs to disease pathogenesis.

Methods

Patient samples, PCR amplification and Sanger sequencing

Tumor biopsy specimens prior to treatment were obtained from 302 patients with de novo DLBCL, which have previously been classified by gene expression profiling, and 116 patients with follicular lymphoma (FL); 75 patients with chronic lymphocytic leukemia (CLL); 68 patients with Hodgkin lymphoma (HL). All samples were studied according to a protocol approved by the National Cancer Institute Institutional Review Board. Genomic DNA from patient samples was extracted with the DNeasy Tissue kit (Qiagen) according to the manufacturer's instructions. The primers used to amplify RNF31 exon 10 are: RNF31_E10_F, 5'-CTGGGCTGGGTGCCTTTTCCTGTCAGG-3' and RNF31_E10_R, 5'-GAGTAATTCTTGGACCAGGTATCG-3'. The PCR products were purified using the MinElute 96 UF PCR Purification Kit (Qiagen) and subsequently sequenced using BigDye sequencing system (Applied Biosystems) from both strands.

Cell Culture

ABC and GCB derived DLBCL cell lines: BJAB, HT, HBL1, DLBCL2, TMD8, OYB, SUDHL2 and TK were grown in RPMI-1640 medium (Invitrogen) +10%FBS (Hyclone, Defined) +pen/strep (Invitrogen); OCI-Ly3, OCI-Ly10, OCI-Ly8 and OCI-Ly19 cell lines were grown in IMDM medium (Invitrogen) +20% human serum +pen/strep (Invitrogen). All cell lines were grown to log phase at 37°C, 5% CO₂ when experiments started. All cell lines had previously been modified to express an ecotropic retroviral receptor and a fusion protein of the Tet repressor and the blasticidin resistance gene, as described previously(5).

Cell lines

ABC DLBCL and GCB DLBCL cell lines were obtained from the following sources: Martin Dyer (HBL1)(45); Hans Messner (OCI-Ly3, OCI-Ly8, OCI-Ly10, OCI-Ly19)(46); Shuji Tohda (TMD8)(47); Momoko Nishikori (OYB, DLBCL2)(48); the JCRB cell bank (TK, <http://cellbank.nibio.go.jp>); ATCC (HT, SUDHL2, <http://www.atcc.org>); and DMSZ (BJAB, <http://www.dsmz.de>). Cell lines have been characterized extensively by gene expression profiling(1) and by cancer gene resequencing(6, 7, 49).

Retroviral vectors and transduction for shRNA expression

The retroviral vectors for shRNA expression were described before(8). In brief, the shRNA oligos were constructed into a pMSCV-based retroviral vector (pRSMX_Puro) constitutive expression of a puromycin resistance marker fused with GFP. The inducible expression of shRNA was released after binding of the bacterial tetracycline repressor by doxycycline (50 ng/ml). For retroviral production, shRNA constructs were mixed with a mutant ecotropic envelope-expressing plasmid pHIT/EA6×3* and gag-pol expressing plasmid pHIT60 and were transfected into 293T cells using the Lipofectamine 2000 reagent (Invitrogen) as described previously(5). The produced retroviral was used to infect doxycycline-inducible lymphoma cells in the presence of 8µg/ml polybrene in a single spin infection and puromycin was used to select for stable integrants over 6 days.

shRNA sequences

Sequences for control and target specific shRNAs are as following: Control shRNA (CTCTCAACCCCTTTAAATCTGA); MYC shRNA (CGATTCCTTCTAACAGAAATG); RNF31 shRNA #3 (GCCAGAGCTGTACCTTTGAGA); RNF31 shRNA #10 (GAAGACAAGGTTGAAGATGAT); SHARPIN shRNA #4 (GGACGCTTGTTCCTCCCATCA); SHARPIN shRNA #6 (GAGCGCAGCCTTGCCTCTTAC).

shRNA toxicity and complementation assays

The toxicity assay of shRNA was described previously(5). In brief, two days after infection with a retrovirus expressing shRNA and GFP, the fraction of GFP positive live cells was measured by Flow Cytometry. Doxycycline was then added to induce shRNA expression, and the fraction of GFP positive live cells was measured at various time points during subsequent culture. The GFP-positive fraction from the test shRNA cultures was normalized to the GFP-positive fraction on day 0.

Retroviral construct used for ectopic expression of RNF31 wild type and mutants was described(8). In brief, the retroviral vector for inducible cDNA expression was pMSCV-based with the cDNA expressed from a doxycycline-inducible cytomegalovirus (CMV) promoter in which a binding site for the bacterial tetracycline repressor is inserted at the transcription start site (derived from pCDNA4/TO (Invitrogen)). The myc tagged human RNF31 cDNA was described(11), and was cloned into retroviral vector for ectopic expression. The RNF31 Q584H and Q622L mutagenesis were performed with the QuikChange kit from Stratagene and verified by Sanger sequencing. For the RNF31 shRNA rescue retroviral constructs, additional mutations were introduced to RNF31 shRNA targeted sequence with the primers:

Forward, p-GCTGTTGGAAGACAAAGTAGAGGATGATATGCTGC;

Reverse, p- GCAGCATATCATCCTCTACTTTGTCTTCCAACAGC.

Antibody and reagents

The antibody against linear ubiquitin chains and RBCK1 were described(13). Other antibodies were purchased as follows: anti-IKKβ, anti-phospho-IKKβ, anti-IκBα, anti-

phospho-I κ B α anti-CARD11 from Cell Signaling Technologies; anti-ubiquitin (P4D1), polyclonal anti-NEMO/IKK γ (FL-419) anti- β -actin, anti-IRAK1, anti-MALT1, anti-A20 from Santa Cruz Biotechnology; anti-RNF31, anti-SHARPIN, anti-myc-tag from Abcam; monoclonal anti-NEMO/IKK γ from BD Pharmingen; anti-human IgM from Jackson ImmunoResearch Lab. Isotype control antibodies were obtained from the same company as each experimental antibody. Secondary HRP-conjugated antibodies were obtained from GE Healthcare.

The Myc-tag elution peptide and Etoposide were obtained from Sigma. The IMiD compound lenalidomide was obtained from Celgene Corporation. The IKK β inhibitor MLN120B was obtained from Millennium Pharmaceuticals. The BTK inhibitor (ibrutinib) was obtained from Pharmacyclics, Inc. The MALT1 inhibitor Z-VRPR-FMK was obtained from Enzo Life Sciences. Tissue culture grade DMSO vehicle control was obtained from Sigma-Aldrich.

Western blotting

Cell pellets were lysed in the modified RIPA buffer (50mM Tris-HCl pH 7.5, 150mM NaCl, 1% NP40, 0.25% deoxycholic acid, 1mM EDTA) supplemented with protease inhibitor tablet and phosphatase inhibitor tablet (Roche), 1mM DTT, 1mM Na₃VaO₄, 1mM PMSF. Protein concentration was measured by BCA Protein Assay Kit (Thermo Scientific). Total proteins were separated on 4% to 12% SDS-polyacrylamide gels and transferred to nitrocellulose membranes.

NEMO immunoprecipitation and ubiquitination

For NEMO ubiquitination, cells were boiled 15 minutes in 1% SDS before immunoprecipitation. Boiled lysates were diluted to 0.1% SDS with a modified RIPA buffer (50mM Tris-HCl pH 7.5, 150mM NaCl, 1% NP40, 0.25% deoxycholic acid, 1mM EDTA, supplemented with protease inhibitors and 5mM N-ethylmaleimide (Sigma)). Cleared lysates were incubated overnight with polyclonal anti-NEMO/IKK γ antibody (Santa Cruz FL-419). Immunoprecipitates were washed 5 times with lysis buffer, separated by SDS-PAGE, transferred to nitrocellulose and analyzed by immunoblotting with an anti-ubiquitin antibody. The method for the detection of NEMO linear polyubiquitination was described(13). In brief, cells were boiled 15 mins in 1% SDS then diluted to 0.1% SDS with a modified RIPA buffer. Cleared lysates were subjected to immunoprecipitation with an anti-NEMO monoclonal antibody (BD pharmingen). Immunoprecipitates were separated on 4% to 12% SDS-polyacrylamide gels and transferred to nitrocellulose membranes, autoclaved with distilled water at 121 degree for 30 min, and then autoclaved again for 15 min without water. Membranes were analyzed by immunoblotting with an anti-linear ubiquitin antibody.

Co-immunoprecipitation

Cells were lysed in an endogenous lysis buffer (20mM Tris-HCl pH 7.6, 150mM NaCl, 1mM EDTA, 1% Triton X-100, 30mM NaF, and 2mM sodium pyrophosphate) supplemented with complete protease inhibitor cocktail (Roche), phosphatase inhibitor tablet (Roche), 1mM DTT, 1mM Na₃VaO₄, 1mM PMSF. Cleared lysates were incubated

overnight with polyclonal anti-MALT, anti-IRAK1 and control antibodies. Immunoprecipitates were washed 5 times with 0.5M NaCl lysis buffer, separated by SDS-PAGE, transferred to nitrocellulose and analyzed by immunoblotting.

E3 ubiquitin ligase assay and *in vitro* ubiquitination assay

Engineered HBL1 lines induced to expression myc- tagged RNF31 various isoforms were lysed in an endogenous lysis buffer (20mM Tris-HCl pH 7.6, 150mM NaCl, 1mM EDTA, 1% Triton X-100, 30mM NaF, and 2mM sodium pyrophosphate) supplemented with complete protease inhibitor cocktail (Roche), phosphatase inhibitor tablet (Roche), 1mM DTT, 1mM Na₃VaO₄, 1mM PMSF. Cleared lysates were incubated overnight with an anti-myc antibody. Immunoprecipitates were washed 5 times with lysis buffer, eluted with myc specific peptides and subjected to E3 ubiquitin ligase assay using E3LITE customizable ubiquitin ligase kit obtained from Life Sensors, following manufacturer's instructions.

For *in vitro* ubiquitination assay, the immunoprecipitated LUBAC complex was washed 5 times with lysis buffer, eluted with myc specific peptides and resuspended in 40 µl of 20 mM Tris/HCl, pH 7.5, 2 mM DTT, 0.1 µM UBE1, 0.4 µM UBCH5C, 10 µM ubiquitin, 5 mM MgCl₂ and 2 mM ATP. Reaction mixtures were incubated for 1 h at 30°C and stopped by boiling 10 minutes with SDS. The formation of linear-ubiquitin chains was analysed by immunoblotting with an anti-ubiquitin antibody.

NF-κB p65 DNA-binding Elisa

NF-κB p65 DNA-binding activity was measured using TransAM NF-κB p65 ELISA kit obtained from Active Motif, following manufacturer's instructions.

IκB kinase activity reporter assay

The assay for IκB kinase activity using the IκBα-photinus luciferase reporter has been described(6). In brief, stable clones of TMD8 were constructed with vectors to express a fusion protein between IκBα and Photinus luciferase (from pGL3; Promega) as the reporter, and Renilla luciferase (from phRL-TK; Promega) for normalization. The ratio of IκBα – Photinus to Renilla luminescence was measured by Dual- Glo luciferase assay system (Promega), and was normalized to that in untreated or uninduced controls.

NF-κB reporter assays

NF-κB transcriptional reporter ABC DLBCL lines were generated by transduction with lentiviral particles containing an inducible NF-κB responsive luciferase reporter construct (SA Biosciences) and selected with puromycin. Luciferase activity was measured using the Dual-Luciferase Reporter Assay System (Promega) on a Microtiter Plate Luminometer (Dyn-Ex Technologies).

Flow cytometry

Flow cytometry for NF-κB activation was performed three days after transgene infected. CD83 expression in BJAB cells was determined by staining with an anti human CD83 antibody (BioLegend).

Peptide synthesis

Peptide synthesis, olefin metathesis, FITC derivatization, reverse-phase HPLC purification, and amino acid analysis were performed as described(50).

Circular dichroism spectroscopy

Peptides (dry, powder form) were dissolved in H₂O to prepare 50 μ M solutions. The spectra were obtained on a Jasco J-715 spectropolarimeter at 20°C. The spectra were collected using a 0.1 cm pathlength quartz cuvette with the following measurement parameters: wavelength, 185-255 nm; step resolution 0.2 nm; speed, 20 nm min⁻¹; accumulations, 3; bandwidth, 1 nm.

Fluorescence polarization assay and competition assay

For binding assays, FITC-peptide ($L_T = 14.1$ nM) was incubated with a broad range of GST-RBCK1 concentrations in 50 mM Tris, 150 mM NaCl, pH 8.0 at 4°C. Binding activity was measured by fluorescence polarization on a Spectramax M5 Microplate Reader (Molecular Devices) in a black, polystyrene, non-treated, 96-well plate (Costar, Corning Inc.), at 20 min. K_d values were determined by nonlinear regression analysis of dose response curves using Prism GraphPad software v 6.0. Each data point represents the average of an experimental condition performed in at least triplicate. For competition assays, FITC-RNF31-N Q2L peptide (14.1 nM) was combined with a serial dilution of unlabeled, Ac-RNF31 N-WT, or Ac-RNF31 N-Q622L peptide, followed by addition of GST-RBCK1 protein (700 nM). IC₅₀ values for FITC-peptide displacement were calculated by nonlinear regression analysis using Prism software (GraphPad).

RBCK1 recombinant protein

The codon optimized cDNA for *E. coli* expression of full length human RBCK1 was a kind gift of Dr. Titia K Sixma (Nijmegen, The Netherlands). To express, the transformed *E. coli* B121 (DE3) pLysS cells were induced with 0.8 mM IPTG and 0.2 mM ZnSO₄ for 8 hours at 22°C. Cells were lysed by using the B-PER bacterial protein extraction reagent (Thermo Scientific) and full length human RBCK1 was purified with Pierce GST spin purification kit (Thermo Scientific).

Confocal microscopy

Images were acquired using a Zeiss LSM510 Meta laser scanning confocal microscope equipped with a 40x C-apochromat (N.A. 1.2) objective lens, transmitted light detector, and differential interference contrast optical components. Confocal fluorescence images were collected with consistent detector settings for all samples, including 0.11 μ m X-Y pixel size, 1.5 μ m optical slice thickness, and 4x frame averaging. The final images were exported as tiff files and arranged into figures using Adobe Photoshop (v.9.0). The brightness and contrast was adjusted equally for all images, using histogram stretching and adjustment of gamma to a value of 1.10.

Cell viability (MTS) assay

Cells were plated in triplicate at a density of 10,000 cells per well in 96-well plates. Cell viability after indicated treatments was assayed by adding MTS reagents (Promega), incubated for 1h and measured by the amount of 490nm absorbance using a 96-well plate reader. The background was subtracted using a media only control.

Statistical analysis

All experiments presented have been repeated and results reproduced. Where possible, error bars or p-values are shown to indicate statistical significance. For SNPs enrichment analysis, two sided p-values for differences in prevalence were calculated using a Fisher's exact test. Confidence levels for the enrichment values were calculated using a normal approximation to the log enrichment. Confidence intervals for prevalence estimates were calculated using the Clopper-Pearson method.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Significance

We provide genetic, biochemical and functional evidence that the LUBAC ubiquitin ligase is a therapeutic target in ABC DLBCL, the DLBCL subtype that is most refractory to current therapy. More generally, our findings highlight the role of rare germ line-encoded protein variants in cancer pathogenesis.

Figure 1. Enrichment of two rare SNPs among ABC DLBCL tumors

a, Amino acid sequence (based on accession NP_060469) of a region of the UBA domain of RNF31 showing the residues altered by two SNPs, Q584H and Q622L, and the number and type of lymphoma biopsies in which they were identified. **b**, Location of RNF31 SNPs in two views of the three-dimensional structure of the RNF31 UBA domain. **c**, Frequencies of RNF31 SNPs in biopsy samples from different lymphoma subtypes.

Figure 2. LUBAC is essential for NF- κ B activity in ABC DLBCL

a, RNF31 and SHARPIN shRNAs are selectively toxic for ABC DLBCL lines. Shown is the fraction of viable GFP⁺, shRNA-expressing cells relative to the total live cell fraction at the indicated times following shRNA induction, normalized to the day 0 values. **b**, Lysates were prepared using 1% SDS from HBL1 ABC DLBCL cells expressing the indicated shRNAs, diluted and then subjected to anti-NEMO immunoprecipitation, followed by immunoblotting for indicated proteins (left). Relative NEMO ubiquitination signal intensity was determined by densitometric analysis (middle). Lysates were additionally analyzed by immunoblotting for the indicated proteins (right). **c**, Relative IκBα-luciferase reporter activity in TMD8 ABC DLBCL cells induced for various days to express the indicated shRNAs. A specific IKKβ inhibitor (MLN120B; 10 μM) was included as a positive control. **d**, Nuclear fractions prepared from HBL1 cells expressing the indicated shRNAs were assayed for NF-κB p65 DNA-binding activity by ELISA. **e**, Relative activity of an NF-κB-dependent luciferase reporter in the ABC DLBCL lines expressing the indicated shRNAs. All error bars denote SEM of triplicates.

Figure 3. LUBAC involves in CBM complex mediated NF- κ B activation in ABC DLBCL

a, ABC DLBCL lines engineered to express myc epitope-tagged RNF31 were immunoprecipitated using antibodies to IRAK1 or MALT1, or control IgG (ctrl.) and were analyzed by immunoblotting for the indicated proteins. **b**, HBL1 cells were engineered to express the indicated shRNAs, treated with MALT1 inhibitor Z-VRPR-fmk (75 μ M) for 24 hours or left untreated. Whole cells lysate was immunoblotted for indicated proteins. MALT1-dependent A20 cleavage products are indicated. **c**, HBL1 cells expressing the indicated shRNAs were activated by anti-IgM treatment (10 μ g/ml) for indicated times and analyzed by immunoblotting for the indicated proteins. **d**, Viability of ABC DLBCL lines expressing control or RNF31 shRNAs were treated with DMSO, ibrutinib (1 nM) or lenalidomide (2 μ M) and analyzed by FACS for viable GFP+/shRNA-expressing cells over a time course.

Figure 4. RNF31 SNPs promote NF- κ B activity in ABC DLBCL

a, NF- κ B-driven luciferase reporter activity in HBL1 and TMD8 lines engineered to express the indicated myc epitope-tagged RNF31 isoforms. **b**, Control or RNF31 shRNAs were inducibly expressed in HBL1 cells that had been transduced with rescue vectors expressing RNF31 isoforms or with an empty vector. Indicated mRNA expression was quantified by Q-PCR and normalized to β 2-microglobulin mRNA levels. **c**, Relative I κ B α -luciferase reporter activity was measured in TMD8 cells induced to express the indicated myc-tagged RNF31 isoforms. **d**, Cells prepared as in Fig. 4b were analyzed by immunoblotting for the indicated proteins. **e**, Nuclear NF- κ B p65 DNA-binding activity was determined by ELISA in HBL1 cells selected for expression of the indicated myc epitope-tagged RNF31 isoforms. **f**, Flow cytometry histograms of the expression of the NF- κ B target gene CD83 in BJAB cells expressing vector only or the indicated exogenous RNF31 isoforms, with and without anti-IgM stimulation. Right panel: summary of CD83 expression in BJAB cells expressing vector only or RNF31 isoforms, either in unstimulated cells or anti-IgM stimulated cells. **g**, HBL1 cells engineered to express indicated myc epitope-tagged RNF31 isoforms were analyzed by immunoblotting for the indicated proteins (top). The relative A20 cleavage signal intensity was determined by densitometric analysis (bottom). **h**, Cells prepared as in Fig. 4g were subject to anti-MALT1 immunoprecipitation. Immunoprecipitated proteins or whole cell lysates were analyzed by immunoblotting for the indicated proteins. *All error bars denote SEM of triplicates.*

Figure 5. Gain-of-function conferred by RNF31 SNPs

a, Control or RNF31 shRNAs were inducibly expressed in HBL1 cells that had been transduced with rescue vectors expressing RNF31 isoforms or with an empty vector. Dox induced cells were lysed in 1% SDS, diluted and then subjected to immunoprecipitation with an anti-NEMO antibody, followed by immunoblotting for indicated proteins (top). The relative NEMO linear ubiquitination signal intensity was determined by densitometric analysis (bottom). Also shown are immunoblots for the indicated proteins in whole cell lysates from the same cells. **b**, HBL1 cells engineered to express indicated myc epitope-tagged RNF31 isoforms were subject to anti-myc immunoprecipitation followed by elution with myc peptides. The elutions were examined in an E3 ligase activity ELISA assay (top) or by immunoblotting for the indicated proteins. **c**, Protein prepared as in Fig. 5b were used in an *in vitro* ubiquitination assay, the products of which were analyzed by immunoblotting for the indicated proteins. **d**, Anti-myc immunoprecipitates prepared as in Fig. 5b or whole cell lysates were analyzed by immunoblotting for the indicated proteins. **e**, Densitometric quantitation of co-immunoprecipitation experiments demonstrating the association of RNF31 isoforms and RBCK as in panel 5d. All error bars denote SEM of replicate experiments (n=3 for all experiments except 5e (n=11)).

Figure 6. Targeting RBCK1-RNF31 interface using stapled α -helical RNF31 peptides

a, Schematic and sequences of RNF31 stapled peptides. Asterisks indicate the location of the hydrocarbon crosslinker. **b**, Circular dichroism spectroscopy of RNF31 peptides. Dips in the curves at 205 and 225 nm are indicative of α -helical structure. **c**, Fluorescence polarization assay of FITC-labeled RNF31 peptides (14.1 nM) binding to recombinant RBCK1. **d**, Competitive fluorescence polarization assay in which binding FITC- RNF31 N-Q622L (14.1 nM) to RBCK1 (0.7 μ M) was inhibited by the indicated concentrations of unlabeled peptides.

Figure 7. Biological effects of RNF31 stapled peptides in ABC DLBCL

a, NF-κB-dependent luciferase reporter activity in HBL1 cells treated for 2 days with DMSO or the indicated peptides. Data are normalized to DMSO-treated cells. **b**, IκBα-luciferase reporter activity in TMD8 cells treated for 3 days with DMSO or the indicated peptides. Data are normalized to DMSO-treated cells. **c**, Viability of DLBCL lines treated with stapled RNF31 Q622L peptide at the indicated concentrations +/- ibrutinib (0.5 nM) for 3 days, normalized to DMSO-treated cells. **d**, HBL1 cells prepared as in Fig. 4b were exposed to etoposide (5 μM) or DMSO for 1.5 hours. Whole cells lysates was blotted for the indicated proteins. **e**, Viability of TMD8 cells treated for 4 days with DMSO or the indicated peptides at various concentrations +/- etoposide (100 nM), normalized to viability of DMSO-treated cells. Neg. ctrl.: negative control stapled peptide. All error bars denote SEM of triplicates.